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Details

 ☐ 1: AF068748. Mus musculus sphi...[gi:3659691]

Links

LOCUS AF068748 1815 bp mRNA linear ROD 29-S EP-1998

DEFINITION Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.

ACCESSION AF068748

VERSION AF068748.1 GI:3659691

KEYWORDS

SOURCE Mus musculus

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1815)

AUTHORS Kohama,T., Olivera,A., Edsall,L., Nagiec,M.M., Dickson,R. and
Spiegel,S.TITLE Molecular cloning and functional characterization of murine
sphingosine kinase

JOURNAL J. Biol. Chem. 273 (37), 23722 -23728 (1998)

MEDLINE 98395082

PUBMED 9726979

REFERENCE 2 (bases 1 to 1815)

AUTHORS Kohama,T., Olivera,A., Edsall,L., Nagiec,M.M., Dickson,R. and
Spiegel,S.

TITLE Direct Submission

JOURNAL Submitted (26 -MAY-1998) Biochemistry, Georgetown University, 3900
Reservoir Rd, Washington, DC 20007, USA

FEATURES Location/Qualifiers

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/db_xref="taxon:10090"
/dev_stage="8.5 day embryo"

gene

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/gene="SPHK1a"

CDS

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/codon_start=2
/product="sphingosine kinase"
/protein_id="AAC61697.1"
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TSSSAGAAPVAPCQREPRDLAMEPECP RGLLP RPCRVLVLLNPQGGKGKALQLFQSRV
QPFLEEA EITFKLILTERKNHARELVCAEELGHW DALAVMSGDGLMH EVVNGLMERP D
WETAIQKPLCSLPGGSGNALAASVNHYAGYEQVTNEDLLINCTLLLCRRRLSPMNL L S
LHTASGLRLYSVLSLSWGFVADVDLESEKYRRLGEIRFTVGTFFRLASLR IYQGQLAY
LPVGTVASKRPASTLVQKGPVDTHLVPLEEPVPSHWTVPVEQDFLLVLVLLH LTHLSSE
LFAAPMRGCEAGVMHLFYVRAGVSR AALLRLFLAMQKKGKHMELDCPYLVHVVPVAFRL
EPRSQRGVFSVDGELMVCEAVQGVHPNYLWMVCGSRDAPSGRDSRRGPPPEEP"

BASE COUNT 382 a 511 c 533 g 389 t

ORIGIN

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121  cgttttcctc  ttggactcgc  ctcttctgga  ctttaagaag  cgatgcgaag  atagagatct
181  ggccgccccg  ggaatgacg  agggcgctca  cacagcccag  ggaggtggag  agggcgagcc
241  ccacggccag  tcgccagaca  ccctcctggg  caacaccgat  aagaagctga  acgcaggagc
301  cgccgttacc  tctagcagc  ccggggcagc  accggtggcc  ccttgtcagc  gggagccccg
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1321 ggttcatgtg cccgtggttg ctttccgcct ggagcccagg agccagaggg gcgtgttttc
1381 tgtggatgga gagctgatgg tatgtgaagc tgtgcagggc caagtgcacc caaactacct
1441 ttgatggtc tgtggcagca gagatgcccc atccggccgg gactcccggc gggggccacc
1501 tccagaagaa ccataactct gtgcctttgt ctactctgtc taggctgaga tgggaccttc
1561 ccccgacccc acttcctggt atgggagggt atttctaaag ttctatgga agtgggtggg
1621 acccctgcag agaaagctag aagggtgggc tatgacttgg aaagaaaggc tctaccttcc
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1741 tccccattgc tcttagggac cttccctggg aaccaaattc aaataaagag acttttccaa
1801 aaaaaaaaaa aaaaa
```

//

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1: BI946369.01112 leafy spurg...[gi:16284977]

Links

IDENTIFIERS

dbEST Id: 9916317
EST name: 01112
GenBank Acc: BI946369
GenBank gi: 16284977

CLONE INFO

Clone Id: 31AN (5')
DNA type: cDNA

PRIMERS

Sequencing: pAD5
PolyA Tail: Unknown

SEQUENCE

GGCACGAGGCAAACCTCCAGCTCCCAAATGGATCAATCCGATACCTCGCCGACGACGGCC
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GTCTGTCTGTGGAGGAAGTACCGGASCTTTGGTCAGGAAGGATTTCAATTCCASCCTTG
ACTCAARAATCGGGGAGACTTTGGTGCCAGCATCTCCGTGATTATCTCAATTCTCTCGGY
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GTTTTCTTGATGTTGTAAAACCATTAAGGAARATGCTGATGTCCAATTCACATTGCAA
GAAACTAAACGTCAGCTGCATGCCAAGGAAGTTGCTAAGGTTCTGGATCTAAGTAAATAT
GATGGTATAGT

Entry Created: Oct 19 2001
Last Updated: Oct 19 2001

PUTATIVE ID Assigned by submitter
PIR:T05162 T05162 hypothetical protein F18E5.160 -
Arabidopsis thaliana EMB:O65419 O65419 HYPOTHETICAL 138.7
KDA PROTEIN.

LIBRARY

Lib Name: leafy spurge Lambda HybriZAP 2.1 two-h ybrid vector cDNA
Library
Organism: Euphorbia esula
Tissue type: underground adventitious buds
Develop. stage: 3-day induced (decapitated)

SUBMITTER

Name: Anderson JV
Lab: Plants Science Research
Institution: USDA/ARS, Biosciences Research Lab
Address: 1605 Albrecht Blvd., PO Box 5674, Fargo, ND 58105, USA
Tel: 701 239 1263
Fax: 701 239 1252
E-mail: andersjv@fargo.ars.usda.gov

CITATIONS

Title: Identification of mRNAs expressed in underground
adventitious buds of Euphorbia esula (leafy spurge)
Authors: Anderson, J.V., Horvath, D.P.
Year: 2000
Status: Unpublished

MAP DATA

Revised: July 5, 2002.

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 ☐ 1: AI237625. EST234187 Normali...[gi:3831131]

Links

IDENTIFIERS

dbEST Id: 2010430
EST name: EST234187
GenBank Acc: AI237625
GenBank gi: 3831131

CLONE INFO

Clone Id: RPLDB60 (3' end)
Source: ATCC
Id in host: 2044267
DNA type: cDNA

PRIMERS

Sequencing: M13 -21
PolyA Tail: Unknown

SEQUENCE

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CCAAACTTCTGCTTCTCTAGTTCTTCAAGTCATTGTCATCTTCCACGTGCTTTGAT  
GTGAACTGGAATTTCTTGACTCGATAAACTTCAACGAAAGTGAAGCCAACTGATCCTCC  
TGGTTGGTGTGCCGGATGAGGAATCTCAGGAAGTTGAACCTGGAGCATTTCCGATAAGG  
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Entry Created: Nov 2 1998
Last Updated: Jan 31 1999

LIBRARY

Lib Name: Normalized rat placenta, Bento Soares
Organism: Rattus sp.
Organ: placenta
Vector: pT7T3Pac
R. Site 1: EcoRI
R. Site 2: NotI

SUBMITTER

Name: Lee, NH
Institution: The Institute for Genomic Research
Address: 9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301) -838-3529
Fax: (301) -838-0208
E-mail: nhlee@tigr.org

CITATIONS

Title: Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat Gene Index
Authors: Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R., Adams, M.D.
Year: 1998
Status: Unpublished




MAP DATA

Revised: July 5, 2002.

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☐ 1: NM_059576. Caenorhabditis el...[gi:17509012][Links](#)

LOCUS T10B11.2 1650 bp mRNA linear INV 03-D EC-2001
DEFINITION Caenorhabditis elegans T10B11.2.p (T10B11.2), mRNA.
ACCESSION NM_059576
VERSION NM_059576.1 GI:17509012
KEYWORDS
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 1650)
AUTHORS Annotated by the C.elegans Genome Sequencing Consortium.
TITLE Direct Submission
JOURNAL Submitted (03-DEC-2001) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA
FEATURES Location/Qualifiers
source 1..1650
/organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
gene 1..1650
/gene="T10B11.2"
/db_xref="WormBase: T10B11.2"
CDS 1..1650
/gene="T10B11.2"
/codon_start=1
/product="T10B11.2.p"
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BASE COUNT 524 a 317 c 326 g 483 t
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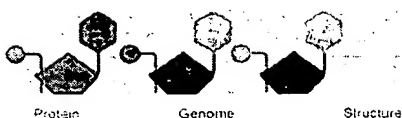
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Search for Limits Preview/Index History Clipboard Details☐ 1: AI478197.tn50c06.x1 NCI_CG...[gi:4371423]

Links

IDENTIFIERS

dbEST Id: 2293388
EST name: tn50c06.x1
GenBank Acc: AI478197
GenBank gi: 4371423

CLONE INFO

Clone Id: IMAGE:2161546 (3')
Source: NCI
Insert length: 591
DNA type: cDNA

PRIMERS

Sequencing: -40UP from Gibco
PolyA Tail: Unknown

SEQUENCE

GGCAGCGCAAGCAAATGTCGCCTTCCCCCTCGCCACCCCGGGGCCGCCGCCGCCAG
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CTCGGGAGGAAGGGGCCGCCACCCGAGCCTCTCCGAGGGGGCGGCGGAGTGCCTAGGG
CGGAGGTGCGACCCTCTTATCTCTTCTCCGAGCGGCTCTTCTCACCTCGTG
CC

Quality: High quality sequence stops at base: 459

Entry Created: Mar 5 1999
Last Updated: Apr 14 1999

COMMENTS

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing
Center
Clone distribution: NCI -CGAP clone distribution information
can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

PUTATIVE ID Assigned by submitter
SW:VNUA_PRVKA P33485 PROBABLE NUCLEAR ANTIGEN. ;contains
MER22.b1 TAR1 TAR1 repetitive element ;

LIBRARY

Lib Name: NCI_CGAP_Kid11
Organism: Homo sapiens
Organ: kidney
Lab host: DH10B
Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker
R. Site 1: Not I
R. Site 2: Eco RI
Description: Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs

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from a pool of 5,000 clones made from the same library
(cloneIDs 1322376 -1323911, 1456007 -1456775, and
1500552 -1502855). Subtraction by Bento Soares and M. Fatima
Bonaldo.

SUBMITTER

Name: Robert Strausberg, Ph.D.
E-mail: cgapbs-r@mail.nih.gov

CITATIONS

Title: National Cancer Institute, Cancer Genome Anatomy Project
(CGAP), Tumor Gene Index
Authors: NCI -CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
Year: 1997
Status: Unpublished



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☐ 1: D31133. HUML12618 Human f...[gi:644013]

[Links](#)

IDENTIFIERS

dbEST Id: 111933
EST name: HUML12618
GenBank Acc: D31133
GenBank gi: 644013

CLONE INFO

Clone Id: (5')
DNA type: cDNA

PRIMERS

PolyA Tail: Unknown

SEQUENCE

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CGGGAGCTGGTGGGTGCGGTGCGAGGAGCTGGGCCGCTGGGACGCTCTGGTGGTCATGTCTGGA  
GACGGGCTGATGCACGAGGTGGTGAACGGGCTCATGGAGCGGCTGACTGGGAGACCGCC  
ATCCAGAAGCCCCTGTNTAGCCTCCCAGCAG
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Entry Created: Feb 8 1995
Last Updated: Feb 8 1995

LIBRARY

Lib Name: Human fetal lung
Organism: Homo sapiens

SUBMITTER

Name: Yusuke Nakamura
Lab: Institute of Medical Science
Institution: University of Tokyo
Address: 4 -6-1, Shirokanedai, Minato -ku, Tokyo 108, Japan
Tel: 81 -3-5449-5372
Fax: 81 -3-5449-5433
E-mail: yusuke@ims.u-tokyo.ac.jp

CITATIONS

Medline UID: [95213017](#)
Title: 2058 expressed sequence tags (ESTs) from a human fetal lung
cDNA library
Authors: Sudo,K., Chinen,K., Nakamura,Y.
Citation: Genomics 24: 276 -279 1995

MAP DATA

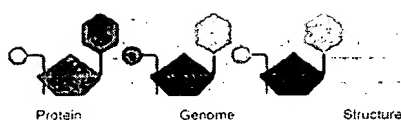
Revised: July 5, 2002.

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☐ 1: AA026479. zj99b03.r1 Soares...[gi:1492691]

Links

IDENTIFIERS

dbEST Id: 640696
EST name: zj99b03.r1
GenBank Acc: AA026479
GenBank gi: 1492691
GDB Id: 3755135

CLONE INFO

Clone Id: IMAGE:469133 (5')
Source: IMAGE Consortium, LLNL
Insert length: 1208
DNA type: cDNA

PRIMERS

Sequencing: -28M13 rev2 from Amersham
PolyA Tail: Unknown

SEQUENCE

NCGCCATCCAGAAGCCCTGTGTAGCCTCCCAGCAGGCTCTGGCAACGCGCTGGCAGCTT
CCTTGAACCATTTATGCTGGCTATGAGCAGGTACCAATGAAGACCTCCTGACCAACTGCA
CGCTATTGCTGTNCCGCCGNTGCTGTACCCATGAACCTGCTGTCTCTGCACACGGCTTC
GGGGCTGCGCTCTTCTCTGTGCTCAGCCTGGCCTGGGGCTTCATGTCTGATGTGGACCTA
GAGAGTGATAAGTATCGGCGCTCTGGGGGAGATGCGCTTCACTCTGGGCACCTTCCCTGCG
TCTGGGCAGCCCTGNGCACCTAANC GCGGCCGACNTGGCT

Quality: High quality sequence stops at base: 165

Entry Created: Jul 23 1996
Last Updated: May 9 1997

COMMENTS

This clone is available royalty -free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

LIBRARY

Lib Name: Soares_pregnant_uterus_NbHPU
Organism: Homo sapiens
Sex: female
Organ: uterus
Develop. stage: adult
Lab host: DH10B
Vector: pT7T3 -Pac
R. Site 1: Not I
R. Site 2: Eco RI
Description: 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGGAAGAATTCGCGGCCGCTTTTTTTTTTTTTTTT 3'], double -stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonáldo.

SUBMITTER

Name: Wilson RK
Institution: Washington University School of Medicine
Address: 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
E-mail: est@watson.wustl.edu



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CITATIONS

Medline UID: [97044478](#)
Title: Generation and analysis of 280,000 human expressed sequence tags
Authors: Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R., Marra, M.
Citation: Genome Res. 6 (9): 807 -828 1996

MAP DATA

Revised: July 5, 2002.

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 ☐ 1: AA232791.zr45f08.r1 Soares...[gi:1855784]

Links

IDENTIFIERS

dbEST Id: 872129
EST name: zr45f08.r1
GenBank Acc: AA232791
GenBank gi: 1855784
GDB Id: 5428407

CLONE INFO

Clone Id: IMAGE:666375 (5')
Source: IMAGE Consortium, LLNL
Insert length: 1252
DNA type: cDNA

PRIMERS

Sequencing: -28m13 rev2 ET from Amersham
PolyA Tail: Unknown

SEQUENCE

CAGGCTCTGGCAACGCGCTGGCAGCTTCCTTGAACCAATTATGCTGGCTATGAGCAGGTCA
CCAATGAAGACCTCCTGACCAACTGCACGCTATTGCTGTGCGCCGGTGCTGCACCCATG
AACCTGCTGCTCTGCACACGGCTTCGGGGCTGCGCTCGTTCTCTGTGCTCAGCCTGGCC
TGGGGCTTCGATTGCTGATGTGGACCTAGAGAGTGAGAAGTATCGGCGTCTGGGGGAGAT
GCGCTTCACTCTGGGCACCTTCCTGCGTCTGGCAGCCCTGCGCACCTACCGCGGCCGACT
GGCTACCTCCCTGTAGGAAGAGTGGGTCCAAGACACCTGCCTCCCCCGTTGTGGTCCAG
CAGGGCCCCGGGTAGATGCACACCTTG

Quality: High quality sequence stops at base: 362

Entry Created: Nov 27 1996
Last Updated: Aug 6 1997

COMMENTS

This clone is available royalty -free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

LIBRARY

Lib Name: Soares_NhHMPu_S1
Organism: Homo sapiens
Organ: mixed (see below)
Tissue type: Pooled human melanocyte, fetal heart, and pregnant uterus
Lab host: DH10B
Vector: pT7T3D -Pac (Pharmacia) with a modified polylinker
R. Site 1: Not I
R. Site 2: Eco RI
Description: Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232 -265223, 340488 -345479, and 484488-4 89479.

SUBMITTER

Name: Wilson RK
Institution: Washington University School of Medicine
Address: 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

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E-mail: est@watson.wustl.edu

CITATIONS

Title: WashU -Merck EST Project 1997
Authors: Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost
,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising
,B., White,Y., Wylie,T., Waterston,R., Wilson,R.
Year: 1997
Status: Unpublished

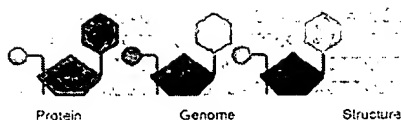
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Revised: July 5, 2002.

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 ☐ 1: AI769914. wj30d06.x1 NCI_CG...[gi:5236423]

Links

IDENTIFIERS

dbEST Id: 2724987
EST name: wj30d06.x1
GenBank Acc: AI769914
GenBank gi: 5236423

CLONE INFO

Clone Id: IMAGE:2404331 (3')
Source: NCI
Insert length: 1211
DNA type: cDNA

PRIMERS

Sequencing: -40UP from Gibco
PolyA Tail: Unknown

SEQUENCE

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TTTGGGAATGTTACTTTATTGATTGTTGTTTCGTGGGGTGGGGGTCTCAAAACAACTAA
AAGGCCTTACATAGGCAGCTGGGCCAGCCAGCTGGGCTCCTGACCCAGGACTTCATTCT
GGCCTGTCCCCCAAAGCATAGCCTCCACCTTCTCACCCCTTCTCCAGAGGAGTCTCCTCC
ACCCCCACAGGAGCTGTGGACAGGCCCTGCAGCCCTAGGGAAGGAGGAAGGGTCTGCAA
GTAAACACTAAGGCACAACGCGGCCAGGGGTCTAAGGGCTCTTCTGGCGGTGGCATCT
GCTGGGGCTTCCAGCTGGGCGGGGGTCCACGCAACCGCTGACCATCCAGAAGTAGTTTG
GGTGACCTGGCCCTGCACGGCCTCGCTAACCATCAATTCCCCATCCACTGCAAAACAGAC
CTTTCCTATCCTTGGGCTCCAAGCGGAAGGCGACACGGGCACATATACCAAGTAGGGGC
ATTCACTATCCATATGCCTGCCCTTCTCCATGGCCAGGAAGAGGCGCAGCAGCATGGCAC
GAGACACTCCCGCCCGCAGTAGAACAGATGCATGACGCCAGCTGCACAGCGGCCATGG
GTGCAGCAAACATCTCACTGGCCAGGTGCGAGTGCAGCAGTGCCAGGACTAGCACAAGT
TCTCGTCGGGCACACCTGTCACTGAGAAGGCACCTGCTCCTCCAGTGGCACCAGGTGTG
CATCTACGGGGCCCTGCTGGACCACACNCGGGAAGCANGTGTCTTGAAC
```

Quality: High quality sequence stops at base: 467

Entry Created: Jun 28 1999
Last Updated: Dec 21 1999

COMMENTS

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Michael R. Emmert -Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing
Center
Clone distribution: NCI -CGAP clone distribution information
can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

PUTATIVE ID Assigned by submitter
TR:088886 088886 SPHINGOSINE KINASE. ;

LIBRARY

Lib Name: NCI_CGAP_Kid12
Organism: Homo sapiens
Organ: kidney
Tissue type: 2 pooled tumors (clear cell type)
Lab host: DH10B
Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker
R. Site 1: Not I
R. Site 2: Eco RI
Description: Plasmid DNA from the normalized library NCI_CGAP_Kid5 was

4.
)

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prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1323912 -1325831, 1471368 -1472903 and 1492104 -1493255). Subtraction by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: Robert Strausberg, Ph.D.
E-mail: cgapbs-r@mail.nih.gov

CITATIONS

Title: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Authors: NCI -CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
Year: 1997
Status: Unpublished




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Revised: July 5, 2002.

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☐ 1: AI972156. wr63c05.x1 NCI_CG...[gi:5768982]

Links

IDENTIFIERS

dbEST Id: 3098238
EST name: wr63c05.x1
GenBank Acc: AI972156
GenBank gi: 5768982

CLONE INFO

Clone Id: IMAGE:2492360 (3')
Source: NCI
Insert length: 1774
DNA type: cDNA

PRIMERS

Sequencing: -40UP from Gibco
PolyA Tail: Unknown

SEQUENCE

```
TTTTGGGAATGTCACTTTATTGGATTGGTTTCGTGGGGTGGGGTCTCAGAACAACTA
GAAGGCCTTACATAGGCAGCTGGGCCCAGCCAGCTGGGCTCCTGACCCAGGACTTCATTC
TGGCCTGTCCCCCAAAGCATAGCCTCCACCTTCTCACCTTCTCCAGAGGAGTCTCCTC
CACCCCCACAGGAGCTGTGGACAGGCCCTGCAGCCCTAGGGAAGGAGGAAGGGTCTTGCA
AGTAGACACTAAGGCACAGCGCGGCCAGGGGTCTAAGGGCTCTTCTGGCGGTGGCATC
TGCTGGGGCTTCCAGCTGGGCGNGGCTCCACGCAACCGCTGACCATCCAGAAGTAGTTT
GGGTGCACCTGGCCCTGCACGGCCTCGCTAACCATCAATTNCCCATCCACTGCAAACACA
CCTTTCCCATCTTGGGCTCCAAGCGGAAGGCGACCACGGGCACATATACCAAGTAGGNG
CATTACTACTCCATATGCCTGCCCTTCTNCATGGCCAGNAAGAGGCGCAGCAGCATGGCA
CGAGACACTCCCCGCCGACGTAGAACAGATGCATGACGCCAGCTGCACAGCGGCCCATG
GGTGCAGCAAACATCTCACTGGCCAGGTGCGAGTGCAG
```

Quality: High quality sequence stops at base: 333

Entry Created: Aug 25 1999
Last Updated: Mar 8 2000

COMMENTS

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Michael R. Emmert -Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing
Center
Clone distribution: NCI -CGAP clone distribution information
can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

PUTATIVE ID Assigned by submitter
TR:O88886 O88886 SPHINGOSINE KINASE. ;

LIBRARY

Lib Name: NCI_CGAP_Ut1
Organism: Homo sapiens
Organ: uterus
Tissue type: well-differentiated endometrial adenocarcinoma, 7 pooled
tumors
Lab host: DH10B
Vector: pCMV-SPORT6
R. Site 1: Sall
R. Site 2: NotI
Description: Cloned unidirectionally. Primer: Oligo dT. Average insert
size 1.75 kb. Life Technologies catalog #: 11538-0 14

SUBMITTER

Name: Robert Strausberg, Ph.D.
E-mail: cgapbs-r@mail.nih.gov

CITATIONS



Title: National Cancer Institute, Cancer Genome Anatomy Project
(CGAP), Tumor Gene Index
Authors: NCI -CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
Year: 1997
Status: Unpublished

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Revised: July 5, 2002.

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☐ 1: AA081152. zn34a06.r1 Strata...[gi:1623227]

Links

IDENTIFIERS

dbEST Id: 716400
EST name: zn34a06.r1
GenBank Acc: AA081152
GenBank gi: 1623227
GDB Id: 3927815

CLONE INFO

Clone Id: IMAGE:549298 (5')
Source: IMAGE Consortium, LLNL
Insert length: 761
DNA type: cDNA

PRIMERS

Sequencing: -28M13 rev2 from Amersham
PolyA Tail: Unknown

SEQUENCE

```
CACNGAGGACTTTGTGCTAGTCCTGGCACTGCTGCACTCGCACCTGGGCAGTGAGATGTT
TGCTGCACCCATGGGCGCTGTGCAGCTGGCGTCATGCATCTGTTCTACGTGCGGGCGGG
AGTGTCTCGTGCCATGCTGCTGCGCCTCTTCCTGGCCATGGAGAAGGGCAGGCATATGGA
GTATGAATGCCCTACTTGGTATATGTGCCCGTGGTCGCCTTCCGCTTGAAGCCCAAGG
AATGGGAAAAGGTGTGTTTGCAAGTGGATGGGAATTGATGGTTAGCGAGGCCGTGCAAG
GGCAAGGTTGCACCCAACTACTTCTTGATGGTCAGCGGTTGCGTTGGAACCCCC
```

Entry Created: Jul 18 1996
Last Updated: Dec 1 1996

COMMENTS

This clone is available royalty -free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

LIBRARY

Lib Name: Stratagene endothelial cell 937223
Organism: Homo sapiens
Develop. stage: umbilical vein, 1 passage
Lab host: SOLR (kanamycin resistant)
Vector: pBluescript SK -
R. Site 1: EcoRI
R. Site 2: XhoI
Description: Cloned unidirectionally. Primer: Oligo dT. Umbilical vein endothelial cells, passaged once. Average insert size: 1.0 kb; Uni -ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'

SUBMITTER

Name: Wilson RK
Institution: Washington University School of Medicine
Address: 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
E-mail: est@watson.wustl.edu

CITATIONS

Medline UID: [97044478](#)
Title: Generation and analysis of 280,000 human expressed sequence tags

Authors: Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C.,
Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F.,
Thierry-Mieg, J., Trevaskis, E., Underwood, K., Wohldmann, P.,
Waterston, R., Wilson, R., Marra, M.

Citation: Genome Res. 6 (9): 807 -828 1996

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Revised: July 5, 2002.

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☐ 1: AL096766. Human DNA sequenc...[gi:5738627]

Links

LOCUS HSDA59H18 70890 bp DNA linear PRI 07-J AN-2000

DEFINITION Human DNA sequence from clone 59H18 on chromosome 22. Contains the 3' part of the gene for KIAA0767, a novel gene, ESTs, STSs, GSSs and a putative CpG island, complete sequence.

ACCESSION AL096766

VERSION AL096766.12 GI:5738627

KEYWORDS HTG; CpG Island; KIAA0767.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 70890)

AUTHORS Bates, K.

TITLE Direct Submission

JOURNAL Submitted (05 -OCT-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

COMMENT On Aug 18, 1999 this sequence version replaced gi: 5734408.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr22>

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep

IMPORTANT: This sequence is not the entire insert of clone 59H18. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true right end of clone 439F8 (AL021392) is at 100 in this sequence. 59H18 is from the library RPCI-6 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/> VECTOR: pPAC4.

FEATURES Location/Qualifiers

source

 1..70890
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="22"
 /clone="59H18"
 /clone_lib="RPCI -6"

misc_feature

 1..877
 /note="Tandem repeat. The assembly in this region is consistent with the digest."

repeat_region

 1..264
 /note="66 copies 4 mer gatg 74% conserved"

repeat_region

10..269

```

repeat_region    /note="5 copies 52 mer 76% conserved"
                  13..268
repeat_region    /note="16 copies 16 mer 73% conserved"
                  13..264
repeat_region    /note="9 copies 28 mer 73% conserved"
                  15..254
repeat_region    /note="6 copies 40 mer 75% conserved"
                  426..545
repeat_region    /note="3 copies 40 mer 75% conserved"
                  555..866
repeat_region    /note="78 copies 4 mer gatg 95% conserved"
                  555..862
repeat_region    /note="11 copies 28 mer 96% conserved"
                  555..858
repeat_region    /note="19 copies 16 mer 96% conserved"
                  568..879
repeat_region    /note="6 copies 52 mer 93% conserved"
                  568..847
repeat_region    /note="7 copies 40 mer 97% conserved"
                  1551..1897
misc_feature     /note="match: GSS: Em:B13877"
                  1677..2176
misc_feature     /note="match: GSS: Em:AQ506837"
                  1684..2116
misc_feature     /note="match: GSS: Em:AQ708634"
                  2177..2326
repeat_region    /note="6 copies 25 mer 91% conserved"
                  3927..4383
repeat_region    /note="MLT1D repeat: matches 1..505 of consensus"
                  5121..5224
repeat_region    /note="2 copies 52 mer 94% conserved"
                  6832..7316
repeat_region    /note="L2 repeat: matches 2068..2542 of consensus"
                  8624..9082
misc_feature     /note="match: GSS: Em:AQ372111"
                  8762..8842
repeat_region    /note="3 copies 27 mer 99% conserved"
                  9337..9385
repeat_region    /note="MLT1D repeat: matches 261..312 of consensus"
                  9391..9572
repeat_region    /note="L2 repeat: matches 2348..2535 of consensus"
                  10055..31655
gene             /gene="dA59H18.1"
mRNA             join(10055..10175,13249..13310,14908..15040,15706..15731,
                  15894..15985,17483..17574,18693..18741,19964..20035,
                  20557..20600,20667..20776,24711..24865,25538..25682,
                  26525..26618,27336..27420,28468..28536,29015..31655)
                  /gene="dA59H18.1"
                  /product="dA59H18.1 (KIAA0767 protein)"
                  /note="match: cDNAs: Em:AB018310
                  match: ESTs: Em:AI092570 Em:AA103568 Em:H11873 Em:H55444
                  Em:AI279741 Em:H45850 Em:AI268624 Em:AI128752 Em:AA830080
                  Em:AI689749 Em:AI310136 Em:AI651233 Em:AI376926 Em:T89772
                  Em:AI201798 Em:AI925374 Em:AI916869 Em:R12734 Em:AI373013
                  Em:AI201646 Em:AA551691 Em:AI342527 Em:AI073809
                  Em:AI857492 Em:AI399959 Em:AI884898 Em:AA053921
                  Em:AI625017 Em:AA034430 Em:AA769084 Em:AI435899 Em:D19781
                  Em:AA287765 Em:AI363150 Em:Z41746 Em:AI580064 Em:R18977
                  Em:R39786 Em:AA417669 Em:AI274949 Em:AI751948 Em:R44862"
                  /evidence=not_experimental
CDS              join(<10055..10175,13249..13310,14908..15040,
                  15706..15731,15894..15985,17483..17574,18693..18741,
                  19964..20035,20557..20600,20667..20776,24711..24865,
                  25538..25682,26525..26618,27336..27420,28468..28536,
                  29015..29119)
                  /gene="dA59H18.1"
                  /codon_start=3
                  /evidence=not_experimental
                  /product="dA59H18.1 (KIAA0767 protein)"
                  /protein_id=" CAB62976.1"
                  /db_xref="GI:6572329"
                  /translation="EELRKLREETNAEMLRQELDRERQRRMELEQKVQEVLKARTEEQ
                  MAQQPPKGQAQASNGAERRSQGLSSRLQKWFYERFGEYVEDFRFQPEENTVETEPEPLS
                  ARRLTENMRRLKRGAKPVTNFVKNLSALSDWYSVYTSIAIFTVMYNAVWHGWAIPFLF
                  FLAILRLSLNYLIARGWRIQWSIVPEVSEPPPKEDLTVSEKQQLVLDVAQKAQNLF

```

GKMADILEKIKNLFMWVQPEITQKLYVALWAAFLASCFFPYRLVGLAVGLYAGIKFFL
IDFIFKRCPRRLRAKYDTPYIIWRSLPTDPQLKERSAAVSRRLQTTSSRSYVPSAPAG
LGKEEDAGRPHSTKKGNFHEIFNLTENERPLAVCENGWRCCLINRDRKMPTDYIRNGV
LYVTENYLCFESSKSGSSKRNVIKLVDITDIQKYKVLSPGSGMGIADVSTPSTQKP
LVFGAMVHRDEAFETILSQYIKITSAAASGGDS"

repeat_region 10098..10169
/note="12 copies 6 mer gctgga 72% conserved"

repeat_region 11004..11281
/note="139 copies 2 mer cc 55% conserved"

repeat_region 11004..11227
/note="8 copies 28 mer 62% conserved"

repeat_region 11011..11130
/note="3 copies 40 mer 92% conserved"

repeat_region 11041..11142
/note="3 copies 34 mer 77% conserved"

repeat_region 13889..13976
/note="MER58 repeat: matches 126..216 of consensus"

repeat_region 15365..15464
/note="L2 repeat: matches 2609..2710 of consensus"

repeat_region 16115..16191
/note="MIR repeat: matches 119..194 of consensus"

misc_feature 16998..17428
/gene="dA59H18.1"
/note="match: GSS: Em:AQ589694"

misc_feature 17084..17413
/gene="dA59H18.1"
/note="match: STS: Em:B18088"

repeat_region 19139..19235
/note="AluSg/x repeat: matches 214..310 of consensus"

repeat_region 19237..19401
/note="MER58A repeat: matches 29..206 of consensus"

repeat_region 20051..20118
/note="2 copies 34 mer 93% conserved"

repeat_region 21370..21433
/note="L1M3c repeat: matches 1243..1304 of consensus"

repeat_region 21434..21746
/note="AluYb8 repeat: matches 1..316 of consensus"

repeat_region 21747..21813
/note="L1M3c repeat: matches 1169..1243 of consensus"

repeat_region 22481..22770
/note="AluSg repeat: matches 1..289 of consensus"

repeat_region 23131..23309
/note="AluSq/x repeat: matches 3..249 of consensus"

repeat_region 23358..23553
/note="AluY repeat: matches 116..311 of consensus"

repeat_region 23555..23712
/note="AluSg/x repeat: matches 120..291 of consensus"

repeat_region 26967..27074
/note="4 copies 27 mer 94% conserved"

repeat_region 27047..27138
/note="4 copies 23 mer 95% conserved"

repeat_region 27116..27196
/note="3 copies 27 mer 94% conserved"

repeat_region 29148..29183
/note="18 copies 2 mer tt 89% conserved"

misc_feature complement(31256..31653)
/note="match: STS: Em:R44862"

misc_feature complement(31347..31546)
/note="match: STS: Em:G43099"

polyA_signal 31628..31633
/gene="dA59H18.1"

polyA_site 31653
/gene="dA59H18.1"

polyA_site 31655
/gene="dA59H18.1"

polyA_site 31659

repeat_region 32409..32828
/note="105 copies 4 mer tcca 85% conserved"

repeat_region 32412..32827
/note="26 copies 16 mer 85% conserved"

repeat_region 32433..32832
/note="10 copies 40 mer 86% conserved"

repeat_region 32433..32796
/note="7 copies 52 mer 87% conserved"

repeat_region 32442..32833

```

repeat_region    /note="14 copies 28 mer 84% conserved"
                 32462..32817
repeat_region    /note="178 copies 2 mer ac 57% conserved"
                 32582..32827
repeat_region    /note="41 copies 6 mer ccaccc 58% conserved"
                 33197..33416
repeat_region    /note="Charlie4 repeat: matches 1718..1957 of consensus"
                 33446..33571
misc_feature     /note="L2 repeat: matches 2090..2216 of consensus"
                 33572..34117
repeat_region    /note="match: EST: Em:AA059372"
                 34697..34942
repeat_region    /note="AluSg repeat: matches 51..295 of consensus"
                 34988..35119
repeat_region    /note="AluJb repeat: matches 1..133 of consensus"
                 35140..35445
repeat_region    /note="AluJb repeat: matches 1..302 of consensus"
                 35622..35939
gene             /note="AluY repeat: matches 1..303 of consensus"
                 complement(join(36277..36716,38462..38586))
mRNA             /gene="dA59H18.3"
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                 Em:AA677192 Em:W67835 Em:W67828 Em:AI075655 Em:AA384221
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repeat_region    /gene="dA59H18.3"
repeat_region    36932..37238
repeat_region    /note="AluSx repeat: matches 1..295 of consensus"
repeat_region    39097..39220
repeat_region    /note="2 copies 62 mer 85% conserved"
repeat_region    39783..40083
repeat_region    /note="AluSq repeat: matches 1..310 of consensus"
repeat_region    41227..41502
repeat_region    /note="AluSx repeat: matches 40..308 of consensus"
repeat_region    42272..42335
repeat_region    /note="4 copies 16 mer 92% conserved"
repeat_region    42785..42928
repeat_region    /note="9 copies 16 mer 72% conserved"
repeat_region    42786..42921
repeat_region    /note="4 copies 34 mer 74% conserved"
repeat_region    42799..42958
repeat_region    /note="40 copies 4 mer atat 69% conserved"
repeat_region    42799..42954
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repeat_region    42803..42958
repeat_region    /note="26 copies 6 mer atat 69% conserved"
repeat_region    42804..42957
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repeat_region    42804..42943
repeat_region    /note="5 copies 28 mer 74% conserved"
repeat_region    42958..43240
repeat_region    /note="AluSx repeat: matches 1..285 of consensus"
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CDS              complement(join(<43440..43645,45295..45371,
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repeat_region 57619..57919
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62320..62525
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repeat_region /note="L1PA5 repeat: matches 5969..6004 of consensus"
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63673..63967
repeat_region /note="AluSg repeat: matches 1..293 of consensus"
64701..64924
repeat_region /note="AluY repeat: matches 88..311 of consensus"
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repeat_region /note="AluSx repeat: matches 1..306 of consensus"
66163..66303
repeat_region /note="AluJb repeat: matches 132..274 of consensus"
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repeat_region /note="L1M4 repeat: matches 3307..4378 of consensus"
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repeat_region /note="AluJo repeat: matches 124..312 of consensus"
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repeat_region /note="AluSx repeat: matches 1..299 of consensus"
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68525..68838
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Revised: July 5, 2002.

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Oct 31 2012 16:00:17

for

☐ 1: CAB62977. dA59H18.2 (novel ...[gi:6572330]

Links

LOCUS CAB62977 326 aa linear PRI 07-J AN-2000
 DEFINITION dA59H18.2 (novel protein similar to human, mouse, yeast, worm and plant (predicted) proteins) [Homo sapiens].
 ACCESSION CAB62977
 VERSION CAB62977.1 GI:6572330
 DBSOURCE embl locus HSDA59H18, accession [AL096766.12](#)
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (residues 1 to 326)
 AUTHORS Bates, K.
 TITLE Direct Submission
 JOURNAL Submitted (05 -OCT-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
 COMMENT This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.
 This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr22>
 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep IMPORTANT: This sequence is not the entire insert of clone 59H18. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
 The true right end of clone 439F8 (AL021392) is at 100 in this sequence. 59H18 is from the library RPCI-6 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/> VECTOR: pPAC4.
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NCBI Sequence Viewer

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 Tr:O14159 Sw:O46641"

ORIGIN

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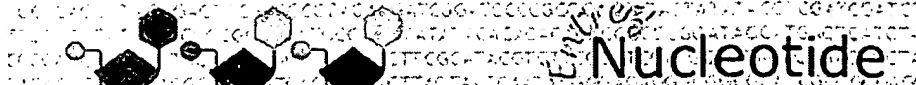

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Revised: July 5, 2002.

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Nucleotide

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☐ 1: AI237625. EST234187 Normali...[gi:3831131]

Links

IDENTIFIERS

dbEST Id: 2010430
EST name: EST234187
GenBank Acc: AI237625
GenBank gi: 3831131

CLONE INFO

Clone Id: RPLDB60 (3' end)
Source: ATCC
Id in host: 2044267
DNA type: cDNA

PRIMERS

Sequencing: M13 -21
PolyA Tail: Unknown

SEQUENCE

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Entry Created: Nov 2 1998
Last Updated: Jan 31 1999

LIBRARY

Lib Name: Normalized rat placenta, Bento Soares
Organism: Rattus sp.
Organ: placenta
Vector: pT7T3Pac
R. Site 1: EcoRI
R. Site 2: NotI

SUBMITTER

Name: Lee, NH
Institution: The Institute for Genomic Research
Address: 9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301) -838-3529
Fax: (301) -838-0208
E-mail: nhlee@tigr.org

CITATIONS


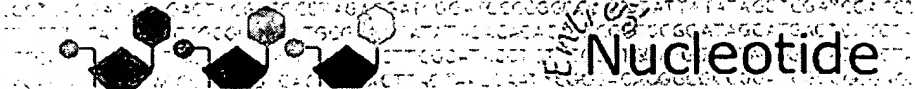
Title: Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat Gene Index
Authors: Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R., Adams, M.D.
Year: 1998
Status: Unpublished

MAP DATA

Revised: July 5, 2002.

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Oct 31 2002 15:09:19

  **Nucleotide**

PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM Bool

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Display default **Save** **Text** **Add to Clipboard**

☐ I: A1536375.mb14a02.y1 Soares...[gi:4450510]

Links

IDENTIFIERS

dbEST Id: 2352535
EST name: mb14a02.y1
GenBank Acc: A1536375
GenBank gi: 4450510

CLONE INFO

Clone Id: IMAGE:329354 (5')
Source: IMAGE Consortium, LLNL
DNA type: cDNA

PRIMERS

Sequencing: -40RP from Gibco
PolyA Tail: no

SEQUENCE

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Entry Created: Mar 18 1999
Last Updated: Mar 15 2000

COMMENTS

This clone is available royalty -free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

This read is a RESEQUENCE of a previously sequenced mouse clone

This read has been verified (found to hit its original self in the correct orientation)

Putative full length read
vector to vector length is 388
MGI:210754

LIBRARY

Lib Name: Soares mouse p3NMF19.5
Organism: Mus musculus
Develop. stage: 19.5 dpc total fetus
Lab host: DH10B (ampicillin resistant)
Vector: pT7T3D (Pharmacia) with a modified polylinker
R. Site 1: Not I
R. Site 2: Eco RI
Description: 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGATTTTTTTTTTTTTTTTTT 3'], double -stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University).

SUBMITTER

Name: Marra M/WashU -NCI Mouse EST Project 1999

NCBI Sequence Viewer

Institution: Washington University School of Medicine
Address: 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
E-mail: mouseest@watson.wustl.edu

CITATIONS

Title: The WashU -NCI Mouse EST Project 1999
Authors: Maïra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie
,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas
,M., McCann,R., Waterston,R., Wilson,R.
Year: 1999
Status: Unpublished

MAP DATA

Revised: July 5, 2002.

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Dec 31 2002 16:00:17